SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: KLEIN, Michel H

 DU, Run-Pan

 EWASYSHYN, Mary E
- (ii) TITLE OF INVENTION: INFECTION DETECTION METHOD USING CHIMERIC PROTEIN
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sim & McBurney
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 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5G 1R7
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/467,961
 - (B) FILING DATE: 06-JUN-1995
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/001,554
 - (B) FILING DATE: 06-JAN-1993
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9200117.1
 - (B) FILING DATE: 06-JAN-1992
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEWART, Michael I
 - (B) REGISTRATION NUMBER: 24,973
 - (C) REFERENCE/DOCKET NUMBER: 1038-1000 MIS:jb
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (416) 595-1155
 - (B) TELEFAX: (416) 595-1163
- (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60 AAGTCAATAC CAACAACTAT TAGCAGTCAT ACGTGCAAGA ACAAGAAAGA AGAGATTCAA AAAGCTAAAT AAGAGAAATC AAAACAAAAG GTATAGAACA CCCGAACAAC AAAATCAAAA 120 180 ACAATGCCAA CTTTAATACT GCTAATTATT ACAACAATGA TTATGGCATC TTCCTGCCAA 240 ATAGATATCA CAAAACTACA GCATGTAGGT GTATTGGTCA ACAGTCCCAA AGGGATGAAG 300 ATATCACAAA ACTTCGAAAC AAGATATCTA ATTTTGAGCC TCATACCAAA AATAGAAGAC 360 TCTAACTCTT GTGGTGACCA ACAGATCAAA CAATACAAGA GGTTATTGGA TAGACTGATC 420 ATCCCTCTAT ATGATGGATT AAGATTACAG AAAGATGTGA TAGTAACCAA TCAAGAATCC 480 AATGAAAACA CTGATCCCAG AACAAGACGA TCCTTTGGAG GGGTAATTGG AACCATTGCT 540 CTGGGAGTAG CAACCTCAGC ACAAATTACA GCGGCAGTTG CTCTGGTTGA AGCCAAGCAG 600 GCAAAATCAG ACATCGAAAA ACTCAAAGAA GCAATCAGGG ACACAAACAA AGCAGTGCAG 660 TCAGTTCAGA GCTCTATAGG AAATTTAATA GTAGCAATTA AATCAGTCCA AGATTATGTC 720 AACAACGAAA TGGTGCCATC GATTGCTAGA CTAGGTTGTG AAGCAGCAGG ACTTCAATTA 780 GGAATTGCAT TAACACAGCA TTACTCAGAA TTAACAAACA TATTTGGTGA TAACATAGGA 840 TCGTTACAAG AAAAAGGAAT AAAATTACAA GGTATAGCAT CATTATACCG CACAAATATC 900 ACAGAAATAT TCACAACATC AACAGTTGAT AAATATGATA TCTATGATCT ATTATTTACA 960 GAATCAATAA AGGTGAGAGT TATAGATGTT GATTTGAATG ATTACTCAAT CACCCTCCAA 1020 GTCAGACTCC CTTTATTAAC TAGGCTGCTG AACACTCAGA TCTACAAAGT AGATTCCATA 1080 TCATATAATA TCCAAAACAG AGAATGGTAT ATCCCTCTTC CCAGCCATAT CATGACGAAA 1140 GGGGCATTTC TAGGTGGAGC AGATGTCAAG GAATGTATAG AAGCATTCAG CAGTTATATA 1200 TGCCCTTCTG ATCCAGGATT TGTACTAAAC CATGAAATGG AGAGCTGCTT ATCAGGAAAC 1260 ATATCCCAAT GTCCAAGAAC CACGGTCACA TCAGACATTG TTCCAAGATA TGCATTTGTC 1320 AATGGAGGAG TGGTTGCAAA CTGTATAACA ACCACCTGTA CATGCAACGG AATCGACAAT 1380

AGAATCAATC	AACCACCTGA	TCAAGGAGTA	AAAATTATAA	CACATAAAGA	ATGTAATACA	1440
ATAGGTATCA	ACGGAATGCT	GTTCAATACA	AATAAAGAAG	GAACTCTTGC	ATTCTACACA	1500
CCAAATGATA	TAACACTAAA	TAATTCTGTT	GCACTTGATC	CAATTGACAT	ATCAATCGAG	1560
CTTAACAAAG	CCAAATCAGA	TCTAGAAGAA	TCAAAAGAAT	GGATAAGAAG	GTCAAATCAA	1620
AAACTAGATT	CTATTGGAAA	CTGGCATCAA	TCTAGCACTA	CAATCATAAT	TATTTTAATA	1680
ATGATCATTA	TATTGTTTAT	AATTAATGTA	ACGATAATTA	CAATTGCAAT	TAAGTATTAC	1740
AGAATTCAAA	AGAGAAATCG	AGTGGATCAA	AATGACAAGC	CATATGTACT	AACAAACAAA	1800
TGACATATCT	ATAGATCATT	AGATATTAAA	ATTATAAAAA	ACTT		1844

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 539 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Thr Leu Ile Leu Leu Ile Ile Thr Thr Met Ile Met Ala Ser 1 5 10 15

Ser Cys Gln Ile Asp Ile Thr Lys Leu Gln His Val Gly Val Leu Val 20 25 30

Asn Ser Pro Lys Gly Met Lys Ile Ser Gln Asn Phe Glu Thr Arg Tyr 35 40 45

Leu Ile Leu Ser Leu Ile Pro Lys Ile Glu Asp Ser Asn Ser Cys Gly 50 55 60

Asp Gln Gln Ile Lys Gln Tyr Lys Arg Leu Leu Asp Arg Leu Ile Ile 65 70 75 80

Pro Leu Tyr Asp Gly Leu Arg Leu Gln Lys Asp Val Ile Val Thr Asn 85 90 95

Gln Glu Ser Asn Glu Asn Thr Asp Pro Arg Thr Arg Arg Ser Phe Gly
100 105 110

Gly Val Ile Gly Thr Ile Ala Leu Gly Val Ala Thr Ser Ala Gln Ile 115 120 125

Thr Ala Ala Val Ala Leu Val Glu Ala Lys Gln Ala Lys Ser Asp Ile 130 135 140

Glu Lys Leu Lys Glu Ala Ile Arg Asp Thr Asn Lys Ala Val Gln Ser

145					150					155					160
Val	Gln	Ser	Ser	Ile 165	Gly	Asn	Leu	Ile	Val 170	Ala	Ile	Lys	Ser	Val 175	Gln
Asp	Tyr	Val	Asn 180	Asn	Glu	Ile	Val	Pro 185	Ser	Ile	Ala	Arg	Leu 190	Gly	Cys
Glu	Ala	Ala 195	Gly	Leu	Gln	Leu	Gly 200	Ile	Ala	Leu	Thr	Gln 205	His	Tyr	Ser
Glu	Leu 210	Thr	Asn	Ile	Phe	Gly 215	Asp	Asn	Ile	Gly	Ser 220	Leu	Gln	Glu	Lys
Gly 225	Ile	Lys	Leu	Gln	Gly 230	Ile	Ala	Ser	Leu	Tyr 235	Arg	Thr	Asn	Ile	Thr 240
Glu	Ile	Phe	Thr	Thr 245	Ser	Thr	Val	Asp	Lys 250	Tyr	Asp	Ile	Tyr	Asp 255	Leu
Leu	Phe	Thr	Glu 260	Ser	Ile	Lys	Val	Arg 265	Val	Ile	Asp	Val	Asp 270	Leu	Asn
Asp	Tyr	Ser 275	Ile	Thr	Leu	Gln	Val 280	Arg	Leu	Pro	Leu	Leu 285	Thr	Arg	Leu
Leu	Asn 290	Thr	Gln	Ile	Tyr	Lys 295	Val	Asp	Ser	Ile	Ser 300	Tyr	Asn	Ile	Gln
Asn 305	Arg	Glu	Trp	Tyr	Ile 310	Pro	Leu	Pro	Ser	His 315	Ile	Met	Thr	Lys	Gly 320
Ala	Phe	Leu	Gly	Gly 325	Ala	Asp	Val	Lys	Glu 330	Cys	Ile	Glu	Ala	Phe 335	Ser
Ser	Tyr	Ile	Cys 340	Pro	Ser	Asp	Pro	Gly 345	Phe	Val	Leu	Asn	His 350	Glu	Met
Glu	Ser	Cys 355	Leu	Ser	Gly	Asn	Ile 360	Ser	Gln	Cys	Pro	Arg 365	Thr	Thr	Val
Thr	Ser 370	Asp	Ile	Val	Pro	Arg 375	Tyr	Ala	Phe	Val	Asn 380	Gly	Gly	Val	Val
Ala 385	Asn	Cys	Ile	Thr	Thr 390	Thr	Cys	Thr	Cys	Asn 395	Gly	Ile	Asp	Asn	Arg 400
Ile	Asn	Gln	Pro	Pro 405	Asp	Gln	Gly	Val	Lys 410	Ile	Ile	Thr	His	Lys 415	Glu
Cys	Asn	Thr	Ile 420	Gly	Ile	Asn	Gly	Met 425	Leu	Phe	Asn	Thr	Asn 430	Lys	Glu
Gly	Thr	Leu 435	Ala	Phe	Tyr	Thr	Pro 440	Asn	Asp	Ile	Thr	Leu 445	Asn	Asn	Ser
Val	Ala	Leu	Asp	Pro	Ile	Asp	Ile	Ser	Ile	Glu	Leu	Asn	Lvs	Ala	Ivs

Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys 480

Leu Asp Ser Ile Gly Asn Trp His Gln Ser Ser Thr Thr Ile Ile Ile Ile Leu Phe Ile Ile Asn Val Thr Ile Ile Ile 500

Thr Ile Ala Ile Lys Tyr Tyr Arg Ile Gln Lys Arg Asn Arg Val Asp 525

Gln Asn Asp Lys Pro Tyr Val Leu Thr Asn Lys

460

455

(2) INFORMATION FOR SEQ ID NO:3:

450

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1833 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGACAAATCC	AAATTCGAGA	TGGAATACTG	GAAGCATACC	AATCACGGAA	AGGATGCTGG	60
CAATGAGCTG	GAGACGTCCA	TGGCTACTAA	TGGCAACAAG	CTCACCAATA	AGATAACATA	120
TATATTATGG	ACAATAATCC	TGGTGTTATT	ATCAATAGTC	TTCATCATAG	TGCTAATTAA	180
TTCCATCAAA	AGTGAAAAGG	CTCATGAATC	ATTGCTGCAA	GACATAAATA	ATGAGTTTAT	240
GGAAATTACA	GAAAAGATCC	AAATGGCATC	GGATAATACC	AATGATCTAA	TACAGTCAGG	300
AGTGAATACA	AGGCTTCTTA	CAATTCAGAG	TCATGTCCAG	AATTATATAC	CAATATCACT	360
GACACAACAG	ATGTCAGATC	TTAGGAAATT	CATTAGTGAA	ATTACAATTA	GAAATGATAA	420
TCAAGAAGTG	CTGCCACAAA	GAATAACACA	TGATGTGGGT	ATAAAACCTT	TAAATCCAGA	480
TGATTTTTGG	AGATGCACGT	CTGGTCTTCC	ATCTTTAATG	AAAACTCCAA	AAATAAGGTT	540
AATGCCAGGG	CCGGGATTAT	TAGCTATGCC	AACGACTGTT	GATGGCTGTA	TCAGAACTCC	600
GTCCTTAGTT	ATAAATGATC	TGATTTATGC	TTATACCTCA	AATCTAATTA	CTCGAGGTTG	660
TCAGGATATA	GGAAAATCAT	ATCAAGTCTT	ACAGATAGGG	ATAATAACTG	TAAACTCAGA	720
CTTGGTACCT	GACTTAAATC	CCAGGATCTC	TCATACTTTT	AACATAAATG	ACAATAGGAA	780
GTCATGTTCT	CTAGCACTCC	TAAATACAGA	TGTATATCAA	CTGTGTTCAA	CTCCCAAAGT	840

TGATGAAAGA TCAGATTATG CATCATCAGG CATAGAAGAT ATTGTACTTG ATATTGTCAA 900 TTATGATGGC TCAATCTCAA CAACAAGATT TAAGAATAAT AACATAAGCT TTGATCAACC 960 TTATGCTGCA CTATACCCAT CTGTTGGACC AGGGATATAC TACAAAGGCA AAATAATATT 1020 TCTCGGGTAT GGAGGTCTTG AACATCCAAT AAATGAGAAT GTAATCTGCA ACACAACTGG 1080 GTGTCCCGGG AAAACACAGA GAGACTGCAA TCAGGCATCT CATAGTCCAT GGTTTTCAGA 1140 TAGGAGGATG GTCAACTCTA TCATTGTTGT TGACAAAGGC TTAAACTCAA TTCCAAAATT 1200 GAAGGTATGG ACGATATCTA TGAGACAGAA TTACTGGGGG TCAGAAGGAA GGTTACTTCT 1260 ACTAGGTAAC AAGATCTATA TATATACAAG ATCCACAAGT TGGCATAGCA AGTTACAATT 1320 AGGAATAATT GATATTACTG ATTACAGTGA TATAAGGATA AAATGGACAT GGCATAATGT 1380 GCTATCAAGA CCAGGAAACA ATGAATGTCC ATGGGGACAT TCATGTCCAG ATGGATGTAT 1440 AACAGGAGTA TATACTGATG CATATCCACT CAATCCCACA GGGAGCATTG TGTCATCTGT 1500 CATATTAGAT TCACAAAAAT CGAGAGTGAA CCCAGTCATA ACTTACTCAA CAGCAACCGA 1560 AAGAGTAAAC GAGCTGGCCA TCCGAAACAG AACACTCTCA GCTGGATATA CAACAACAAG 1620 CTGCATCACA CACTATAACA AAGGATATTG TTTTCATATA GTAGAAATAA ATCAGAAAAG 1680 CTTAAACACA CTTCAACCCA TGTTGTTCAA GACAGAGGTT CCAAAAAGCT GCAGTTAATC 1740 ATAATTAACC GCAATATGCA TTAACCTATC TATAATACAA GTATATGATA AGTAATCAGC 1800 AATCAGACAA TAGACAAAAG GGAAATATAA AAA 1833

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 572 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Tyr Trp Lys His Thr Asn His Gly Lys Asp Ala Gly Asn Glu
1 5 10 15

Leu Glu Thr Ser Met Ala Thr Asn Gly Asn Lys Leu Thr Asn Lys Ile
20 25 30

Thr Tyr Ile Leu Trp Thr Ile Ile Leu Val Leu Leu Ser Ile Val Phe 35 40 45

Ile Ile Val Leu Ile Asn Ser Ile Lys Ser Glu Lys Ala His Glu Ser Leu Leu Gln Asp Ile Asn Asn Glu Phe Met Glu Ile Thr Glu Lys Ile 70 75 Gln Met Ala Ser Asp Asn Thr Asn Asp Leu Ile Gln Ser Gly Val Asn 90 Thr Arg Leu Leu Thr Ile Gln Ser His Val Gln Asn Tyr Ile Pro Ile 105 Ser Leu Thr Gln Gln Met Ser Asp Leu Arg Lys Phe Ile Ser Glu Ile 120 115 Thr Ile Arg Asn Asp Asn Gln Glu Val Leu Pro Gln Arg Ile Thr His 135 Asp Val Gly Ile Lys Pro Leu Asn Pro Asp Asp Phe Trp Arg Cys Thr 150 155 Ser Gly Leu Pro Ser Leu Met Lys Thr Pro Lys Ile Arg Leu Met Pro Gly Pro Gly Leu Leu Ala Met Pro Thr Thr Val Asp Gly Cys Ile Arg 185 Thr Pro Ser Leu Val Ile Asn Asp Leu Ile Tyr Ala Tyr Thr Ser Asn 200 195 Leu Ile Thr Arg Gly Cys Gln Asp Ile Gly Lys Ser Tyr Gln Val Leu Gln Ile Gly Ile Ile Thr Val Asn Ser Asp Leu Val Pro Asp Leu Asn 230 235 Pro Arg Ile Ser His Thr Phe Asn Ile Asn Asp Asn Arg Lys Ser Cys 245 250 Ser Leu Ala Leu Leu Asn Thr Asp Val Tyr Gln Leu Cys Ser Thr Pro 265 Lys Val Asp Glu Arg Ser Asp Tyr Ala Ser Ser Gly Ile Glu Asp Ile Val Leu Asp Ile Val Asn Tyr Asp Gly Ser Ile Ser Thr Thr Arg Phe 295 Lys Asn Asn Asn Ile Ser Phe Asp Gln Pro Tyr Ala Ala Leu Tyr Pro 310 315 Ser Val Gly Pro Gly Ile Tyr Tyr Lys Gly Lys Ile Ile Phe Leu Gly 325 330 Tyr Gly Gly Leu Glu His Pro Ile Asn Glu Asn Val Ile Cys Asn Thr

345

350

340

Thr Gly Cys Pro Gly Lys Thr Gln Arg Asp Cys Asn Gln Ala Ser His 355 360 365

Ser Pro Trp Phe Ser Asp Arg Arg Met Val Asn Ser Ile Ile Val Val 370 375 380

Asp Lys Gly Leu Asn Ser Ile Pro Lys Leu Lys Val Trp Thr Ile Ser 385 390 395 400

Met Arg Gln Asn Tyr Trp Gly Ser Glu Gly Arg Leu Leu Leu Gly
405 410 415

Asn Lys Ile Tyr Ile Tyr Thr Arg Ser Thr Ser Trp His Ser Lys Leu 420 425 430

Gln Leu Gly Ile Ile Asp Ile Thr Asp Tyr Ser Asp Ile Arg Ile Lys 435 440 445

Trp Thr Trp His Asn Val Leu Ser Arg Pro Gly Asn Asn Glu Cys Pro 450 455 460

Trp Gly His Ser Cys Pro Asp Gly Cys Ile Thr Gly Val Tyr Thr Asp 465 470 475 480

Ala Tyr Pro Leu Asn Pro Thr Gly Ser Ile Val Ser Ser Val Ile Leu 485 490 495

Asp Ser Gln Lys Ser Arg Val Asn Pro Val Ile Thr Tyr Ser Thr Ala 500 505 510

Thr Glu Arg Val Asn Glu Leu Ala Ile Arg Asn Arg Thr Leu Ser Ala 515 520 525

Gly Tyr Thr Thr Thr Ser Cys Ile Thr His Tyr Asn Lys Gly Tyr Cys 530 540

Phe His Ile Val Glu Ile Asn Gln Lys Ser Leu Asn Thr Leu Gln Pro 545 550 555 560

Met Leu Phe Lys Thr Glu Val Pro Lys Ser Cys Ser 565 570

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1886 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGCTTTGCTT	CTAGTCAAAA	CATCACTGAA	GAATTTTATC	AATCAACATG	CAGTGCAGTT	120
AGCAAAGGCT	ATCTTAGTGC	TCTAAGAACT	GGTTGGTATA	CTAGTGTTAT	AACTATAGAA	180
TTAAGTAATA	TCAAGGAAAA	TAAGTGTAAT	GGAACAGATG	CTAAGGTAAA	ATTGATGAAA	240
CAAGAATTAG	ATAAATATAA	AAATGCTGTA	ACAGAATTGC	AGTTGCTCAT	GCAAAGCACA	300
CCAGCAGCAA	ACAATCGAGC	CAGAAGAGAA	CTACCAAGGT	TTATGAATTA	TACACTCAAC	360
AATACCAAAA	AAACCAATGT	AACATTAAGC	AAGAAAAGGA	AAAGAAGATT	TCTTGGTTTT	420
TTGTTAGGTG	TTGGATCTGC	AATCGCCAGT	GGCATTGCTG	TATCTAAGGT	CCTGCACTTA	480
GAAGGAGAAG	TGAACAAGAT	CAAAAGTGCT	CTACTATCCA	CAAACAAGGC	CGTAGTCAGC	540
TTATCAAATG	GAGTTAGTGT	CTTAACCAGC	AAAGTGTTAG	ACCTCAAAAA	CTATATAGAT	600
AAACAATTGT	TACCTATTGT	GAATAAGCAA	AGCTGCAGAA	TATCAAATAT	AGAAACTGTG	660
ATAGAGTTCC	AACAAAAGAA	CAACAGACTA	CTAGAGATTA	CCAGGGAATT	TAGTGTTAAT	720
GCAGGTGTAA	CTACACCTGT	AAGCACTTAC	ATGTTAACTA	ATAGTGAATT	ATTGTCATTA	780
ATCAATGATA	TGCCTATAAC	AAATGATCAG	AAAAAGTTAA	TGTCCAACAA	TGTTCAAATA	840
GTTAGACAGC	AAAGTTACTC	TATCATGTCC	ATAATAAAAG	AGGAAGTCTT	AGCATATGTA	900
GTACAATTAC	CACTATATGG	TGTGATAGAT	ACACCTTGTT	GGAAATTACA	CACATCCCCT	960
CTATGTACAA	CCAACACAAA	AGAAGGGTCA	AACATCTGTT	TAACAAGAAC	TGACAGAGGA	1020
TGGTACTGTG	ACAATGCAGG	ATCAGTATCT	TTCTTCCCAC	AAGCTGAAAC	ATGTAAAGTT	1080
CAATCGAATC	GAGTATTTTG	TGACACAATG	AACAGTTTAA	CATTACCAAG	TGAAGTAAAT	1140
CTCTGCAATG	TTGACATATT	CAATCCCAAA	TATGATTGTA	AAATTATGAC	TTCAAAAACA	1200
GATGTAAGCA	GCTCCGTTAT	CACATCTCTA	GGAGCCATTG	TGTCATGCTA	TGGCAAAACT	1260
AAATGTACAG	CATCCAATAA	AAATCGTGGA	ATCATAAAGA	CATTTTCTAA	CGGGTGTGAT	1320
TATGTATCAA	ATAAAGGGGT	GGACACTGTG	TCTGTAGGTA	ACACATTATA	TTATGTAAAT	1380
AAGCAAGAAG	GCAAAAGTCT	CTATGTAAAA	GGTGAACCAA	TAATAAATTT	CTATGACCCA	1440
TTAGTATTCC	CCTCTGATGA	ATTTGATGCA	TCAATATCTC	AAGTCAATGA	GAAGATTAAC	1500
CAGAGTTTAG	CATTTATTCG	TAAATCCGAT	GAATTATTAC	ATAATGTAAA	TGCTGGTAAA	1560
TCAACCACAA	ATATCATGAT	AACTACTATA	ATTATAGTGA	TTATAGTAAT	ATTGTTATCA	1620
TTAATTGCTG	TTGGACTGCT	CCTATACTGT	AAGGCCAGAA	GCACACCAGT	CACACTAAGC	1680
AAGGATCAAC	TGAGTGGTAT	AAATAATATT	GCATTTAGTA	ACTGAATAAA	AATAGCACCT	1740

AATCATGTTC TTACAATGGT TTACTATCTG CTCATAGACA ACCCATCTAT CATTGGATTT 1800

TCTTAAAATC TGAACTTCAT CGAAACTCTT ATCTATAAAC CATCTCACTT ACACTATTTA 1860

AGTAGATTCC TAGTTTATAG TTATAT 1886

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 594 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
- Met Glu Leu Pro Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Ala 1 5 10 15
- Ala Val Thr Phe Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe 20 25 30
- Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu 35 40 45
- Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile 50 55 60
- Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Met Lys 65 70 75 80
- Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu 85 90 95
- Met Gln Ser Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Leu Pro 100 105 110
- Arg Phe Met Asn Tyr Thr Leu Asn Asn Thr Lys Lys Thr Asn Val Thr 115 120 125
- Leu Ser Lys Lys Arg Lys Arg Phe Leu Gly Phe Leu Gly Val 130 135 140
- Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu 145 150 155 160
- Glu Gly Glu Val Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys 165 170 175
- Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
 180 185 190
- Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn 195 200 205

Lys Gln Ser Cys Arg Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln 215 His Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn 230 235 Ala Gly Val Thr Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu 250 Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys 260 265 Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile 280 275 Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro 315 310 Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg 330 325 Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe 345 Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp 360 Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val 375 Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr 385 390 395 Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys 405 410 Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile 425 Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp 435 440 Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro 470 Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn 485 490 Glu Lys Ile Asn Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile

505

510

500

Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Met Ile Thr Thr Ile Ile Glu Ile Glu Ile Ile Val Ile Leu Leu Ser 560 Leu Ile Ala Val Gly Ses Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro 575 Pro Val Thr Leu Ser 580 Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe

Ser Asn

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 920 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGCAAACATG	TCCAAAAACA	AGGACCAACG	CACCGCTAAG	ACACTAGAAA	AGACCTGGGA	60
CACTCTCAAT	CATTTATTAT	TCATATCATC	GGGCTTATAT	AAGTTAAATC	TTAAATCTGT	120
AGCACAAATC	ACATTATCCA	TTCTGGCAAT	GATAATCTCA	ACTTCACTTA	TAATTACAGC	180
CATCATATTC	ATAGCCTCGG	CAAACCACAA	AGTCACACTA	ACAACTGCAA	TCATACAAGA	240
TGCAACAAGC	CAGATCAAGA	ACACAACCCC	AACATACCTC	ACTCAGGATC	CTCAGCTTGG	300
AATCAGCTTC	TCCAATCTGT	CTGAAATTAC	ATCACAAACC	ACCACCATAC	TAGCTTCAAC	360
AACACCAGGA	GTCAAGTCAA	ACCTGCAACC	CACAACAGTC	AAGACTAAAA	ACACAACAAC	420
AACCCAAACA	CAACCCAGCA	AGCCCACTAC	AAAACAACGC	CAAAACAAAC	CACCAAACAA	480
ACCCAATAAT	GATTTTCACT	TCGAAGTGTT	TAACTTTGTA	CCCTGCAGCA	TATGCAGCAA	540
CAATCCAACC	TGCTGGGCTA	TCTGCAAAAG	AATACCAAAC	AAAAAACCAG	GAAAGAAAAC	600
CACCACCAAG	CCTACAAAAA	AACCAACCTT	CAAGACAACC	AAAAAAGATC	TCAAACCTCA	660
AACCACTAAA	CCAAAGGAAG	TACCCACCAC	CAAGCCCACA	GAAGAGCCAA	CCATCAACAC	720

	•					
CACCAAAACA	AACATCACAA	CTACACTGCT	CACCAACAAC	ACCACAGGAA	ATCCAAAAC	r 780
CACAAGTCAA	ATGGAAACCT	TCCACTCAAC	CTCCTCCGAA	GGCAATCTAA	GCCCTTCTC	A 840
AGTCTCCACA	ACATCCGAGC .	ACCCATCACA	ACCCTCATCT	CCACCCAACA	CAACACGCC	A 900
GTAGTTATTA	AAAAAAAA					920
(i) SE ((ATION FOR SE QUENCE CHAR (A) LENGTH: (B) TYPE: am (C) STRANDED (D) TOPOLOGY	ACTERISTICS 298 amino a ino acid NESS: singl	acids			
(xi) SE	QUENCE DESC	RIPTION: SE	EQ ID NO:8:			
Met Se 1	er Lys Asn L 5		Arg Thr Ala	a Lys Thr Le	eu Glu Lys 15	Thr

(xi)	SEQU	JENCI	E DES	SCRII	OIT	J: SE	EQ II	ONO:	8:						
Met 1	Ser	Lys	Asn	Lys 5	Asp	Gln	Arg	Thr	Ala 10	Lys	Thr	Leu	Glu	Lys 15	Thr
Trp	Asp	Thr	Leu 20	Asn	His	Leu	Leu	Phe 25	Ile	Ser	Ser	Gly	Leu 30	Tyr	Lys
Leu	Asn	Leu 35	Lys	Ser	Val	Ala	Gln 40	Ile	Thr	Leu	Ser	Ile 45	Leu	Ala	Met
Ile	Ile 50	Ser	Thr	Ser	Leu	Ile 55	Ile	Thr	Ala	Ile	Ile 60	Phe	Ile	Ala	Ser
Ala 65	Asn	His	Lys	Val	Thr 70	Leu	Thr	Thr	Ala	Ile 75	Ile	Gln	Asp	Ala	Thr 80
Ser	Gln	Ile	Lys	Asn 85	Thr	Thr	Pro	Thr	Tyr 90	Leu	Thr	Gln	Asp	Pro 95	Gln
Leu	Gly	Ile	Ser 100	Phe	Ser	Asn	Leu	Ser 105	Glu	Ile	Thr	Ser	Gln 110	Thr	Thr
Thr	Ile	Leu 115	Ala	Ser	Thr	Thr	Pro 120	Gly	Val	Lys	Ser	Asn 125	Leu	Gln	Pro
Thr	Thr 130	Val	Lys	Thr	Lys	Asn 135	Thr	Thr	Thr	Thr	Gln 140	Thr	Gln	Pro	Ser
Lys 145	Pro	Thr	Thr	Lys	Gln 150	Arg	Gln	Asn	Lys	Pro 155	Pro	Asn	Lys	Pro	Asn 160
Asn	Asp	Phe	His	Phe 165	Glu	Val	Phe	Asn	Phe 170	Val	Pro	Cys	Ser	Ile 175	Cys
Ser	Asn	Asn	Pro 180	Thr	Cys	Trp	Ala	Ile 185	Cys	Lys	Arg	Ile	Pro 190	Asn	Lys

	Lys	Pro	Gly 195	Lys	Lys	Thr	Thr	Thr 200	Lys	Pro	Thr	Lys	Lys 205	Pro	Thr	Phe	
	Lys	Thr 210	Thr	Lys	Lys	Asp	Leu 215	Lys	Pro	Gln	Thr	Thr 220	Lys	Pro	Lys	Glu	
	Val 225	Pro	Thr	Thr	Lys	Pro 230	Thr	Glu	Glu	Pro	Thr 235	Ile	Asn	Thr	Thr	Lys 240	
	Thr	Asn	Ile	Thr	Thr 245	Thr	Leu	Leu	Thr	Asn 250	Asn	Thr	Thr	Gly	Asn 255	Pro	
	Lys	Leu	Thr	Ser 260	Gln	Met	Glu	Thr	Phe 265	His	Ser	Thr	Ser	Ser 270	Glu	Gly	
	Asn	Leu	Ser 275	Pro	Ser	Gln	Val	Ser 280	Thr	Thr	Ser	Glu	His 285	Pro	Ser	Gln	
	Pro	Ser 290	Ser	Pro	Pro	Asn	Thr 295	Thr	Arg	Gln							
(2)	INFO	RMAT:	ION 1	FOR S	SEQ :	ID NO	0:9:										
	(i)	(A) (B) (C)	JENCI) LEI) TYI) STI) TOI	NGTH PE: 1 RAND	: 26 nucle EDNE	base eic a SS: s	e par acid sing:	irs									
	(xi)	SEQ	JENCI	E DES	SCRI	PTIOI	1: S	EQ II	ои о	:9:							
ATCA	ATCA	AA G	GTCC:	rgtg	A TA	ATAG											26
(2)	INFO	RMAT	ION 1	FOR S	SEQ :	ID NO	0:10	:									
	(i)	(A) (B) (C)	UENCI) LEI) TYI) STI) TOI	NGTH PE: 1 RAND	: 17 nucle EDNE:	base eic a SS: s	e par acid sing	irs									
	(xi)	SEQ	JENCI	E DE	SCRI	PTIO	1: S	EQ I	ои о	:10:							
CATG	ACTT	GA T	AATG	AG													17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
AATTCATGGA GTTGCTAATC CTCAAAGCAA ATGCAATTAC CACAATCCTC ACTGCAGTCA	60
CATTTTGTTT TGCTTCTGGT TCTAAG	86
(2) INFORMATION FOR SEQ ID NO:12:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
ACTGGCATCA ATCTAGCACT ACATGAG	27
(2) INFORMATION FOR SEQ ID NO:13:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 136 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
AATTCATGCC AACTTTAATA CTGCTAATTA TTACAACAAT GATTATGGCA TCTTCCTGCC	60
AAATAGATAT CACAAAACTA CAGCATGTAG GTGTATTGGT CAACAGTCCC AAAGGGATGA	120
AGATATCACA AAACTT	136
(2) INFORMATION FOR SEQ ID NO:14: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

(D) TOPOLOGY: linear

ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTC	60
GTAACAGTTT TGTAATAAAA AAACCTATAA ATAG	94
(2) INFORMATION FOR SEQ ID NO:15:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 141 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTC	60
GTAACAGTTT TGTAATAAAA AAACCTATAA ATATTCCGGA ATTCAGATCT GCAGCGGCCG	120
CTCCATCTAG AAGGTACCCG G	141
(2) INFORMATION FOR SEQ ID NO:16: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: CATGACTAAT TCCATCAAAA GTGAAAAGGC T	31
(2) INFORMATION FOR SEQ ID NO:17: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	18
(2) INFORMATION FOR SEQ ID NO:18: (i) SEQUENCE CHARACTERISTICS:	

(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
ATTTCTGTGA TATTTGTGCG GTATAATGAT GCTATACCT	3.9
(2) INFORMATION FOR SEQ ID NO:19:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
CAGGAGAAGG GTATCAAG	18
(2) INFORMATION FOR SEQ ID NO:20:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
AGGAGAAGGG TATCAAG	17
(2) INFORMATION FOR SEQ ID NO:21:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	

ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTC

60

(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(2)	INFORMATION	FOR	SEQ	ID	NO:	:22	:
-----	-------------	-----	-----	----	-----	-----	---

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gln Glu Lys Gly Ile Lys 1 5

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gln Glu Lys Gly Ile Lys 1 5

- (2) INFORMATION FOR SEQ ID NO:24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCAATCTAG CACTACACAG

20

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1617 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCCAACTT TAATACTGCT AATTATTACA ACAATGATTA TGGCATCTTC CTGCCAAATA 60 GATATCACAA AACTACAGCA TGTAGGTGTA TTGGTCAACA GTCCCAAAGG GATGAAGATA 120 TCACAAAACT TCGAAACAAG ATATCTAATT TTGAGCCTCA TACCAAAAAT AGAAGACTCT 180 AACTCTTGTG GTGACCAACA GATCAAACAA TACAAGAGGT TATTGGATAG ACTGATCATC 240 CCTCTATATG ATGGATTAAG ATTACAGAAA GATGTGATAG TAACCAATCA AGAATCCAAT 300 GAAAACACTG ATCCCAGAAC AAGACGATCC TTTGGAGGGG TAATTGGAAC CATTGCTCTG 360 GGAGTAGCAA CCTCAGCACA AATTACAGCG GCAGTTGCTC TGGTTGAAGC CAAGCAGGCA 420 AAATCAGACA TCGAAAAACT CAAAGAAGCA ATCAGGGACA CAAACAAAGC AGTGCAGTCA 480 GTTCAGAGCT CTATAGGAAA TTTAATAGTA GCAATTAAAT CAGTCCAAGA TTATGTCAAC 540 AACGAAATGG TGCCATCGAT TGCTAGACTA GGTTGTGAAG CAGCAGGACT TCAATTAGGA 600 ATTGCATTAA CACAGCATTA CTCAGAATTA ACAAACATAT TTGGTGATAA CATAGGATCG 660 TTACAAGAAA AAGGAATAAA ATTACAAGGT ATAGCATCAT TATACCGCAC AAATATCACA 720 GAAATATTCA CAACATCAAC AGTTGATAAA TATGATATCT ATGATCTATT ATTTACAGAA 780 TCAATAAAGG TGAGAGTTAT AGATGTTGAT TTGAATGATT ACTCAATCAC CCTCCAAGTC 840 AGACTCCCTT TATTAACTAG GCTGCTGAAC ACTCAGATCT ACAAAGTAGA TTCCATATCA 900 TATAATATCC AAAACAGAGA ATGGTATATC CCTCTTCCCA GCCATATCAT GACGAAAGGG 960 GCATTCTAG GTGGAGCAGA TGTCAAGGAA TGTATAGAAG CATTCAGCAG TTATATATGC 1020 CCTTCTGATC CAGGATTTGT ACTAAACCAT GAAATGGAGA GCTGCTTATC AGGAAACATA 1080 TCCCAATGTC CAAGAACCAC GGTCACATCA GACATTGTTC CAAGATATGC ATTTGTCAAT 1140 GGAGGAGTGG TTGCAAACTG TATAACAACC ACCTGTACAT GCAACGGAAT CGACAATAGA 1200 ATCAATCAAC CACCTGATCA AGGAGTAAAA ATTATAACAC ATAAAGAATG TAATACAATA 1260 GGTATCAACG GAATGCTGTT CAATACAAAT AAAGAAGGAA CTCTTGCATT CTACACACCA 1320 AATGATATAA CACTAAATAA TTCTGTTGCA CTTGATCCAA TTGACATATC AATCGAGCTT 1380 AACAAAGCCA AATCAGATCT AGAAGAATCA AAAGAATGGA TAAGAAGGTC AAATCAAAAA 1440 CTAGATTCTA TTGGAAACTG GCATCAATCT AGCACTACAA TCATAATTAT TTTAATAATG 1500 ATCATTATAT TGTTTATAAT TAATGTAACG ATAATTACAA TTGCAATTAA GTATTACAGA 1560 ATTCAAAAGA GAAATCGAGT GGATCAAAAT GACAAGCCAT ATGTACTAAC AAACAAA 1617

⁽²⁾ INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1715 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGAATACT	GGAAGCATAC	CAATCACGGA	AAGGATGCTG	GCAATGAGCT	GGAGACGTCC	60
ATGGCTACTA	ATGGCAACAA	GCTCACCAAT	AAGATAACAT	ATATATTATG	GACAATAATC	120
CTGGTGTTAT	TATCAATAGT	CTTCATCATA	GTGCTAATTA	ATTCCATCAA	AAGTGAAAAG	180
GCTCATGAAT	CATTGCTGCA	AGACATAAAT	AATGAGTTTA	TGGAAATTAC	AGAAAAGATC	240
CAAATGGCAT	CGGATAATAC	CAATGATCTA	ATACAGTCAG	GAGTGAATAC	AAGGCTTCTT	300
ACAATTCAGA	GTCATGTCCA	GAATTATATA	CCAATATCAC	TGACACAACA	GATGTCAGAT	360
CTTAGGAAAT	TCATTAGTGA	AATTACAATT	AGAAATGATA	ATCAAGAAGT	GCTGCCACAA	420
AGAATAACAC	ATGATGTGGG	TATAAAACCT	TTAAATCCAG	ATGATTTTTG	GAGATGCACG	480
TCTGGTCTTC	CATCTTTAAT	GAAAACTCCA	AAAATAAGGT	TAATGCCAGG	GCCGGGATTA	540
TTAGCTATGC	CAACGACTGT	TGATGGCTGT	ATCAGAACTC	CGTCCTTAGT	TATAAATGAT	600
CTGATTTATG	CTTATACCTC	AAATCTAATT	ACTCGAGGTT	GTCAGGATAT	AGGAAAATCA	660
TATCAAGTCT	TACAGATAGG	GATAATAACT	GTAAACTCAG	ACTTGGTACC	TGACTTAAAT	720
CCCAGGATCT	CTCATACTTT	TAACATAAAT	GACAATAGGA	AGTCATGTTC	TCTAGCACTC	780
CTAAATACAG	ATGTATATCA	ACTGTGTTCA	ACTCCCAAAG	TTGATGAAAG	ATCAGATTAT	840
GCATCATCAG	GCATAGAAGA	TATTGTACTT	GATATTGTCA	ATTATGATGG	CTCAATCTCA	900
ACAACAAGAT	TTAAGAATAA	TAACATAAGC	TTTGATCAAC	CTTATGCTGC	ACTATACCCA	960
TCTGTTGGAC	CAGGGATATA	CTACAAAGGC	AAAATAATAT	TTCTCGGGTA	TGGAGGTCTT	1020
GAACATCCAA	TAAATGAGAA	TGTAATCTGC	AACACAACTG	GGTGTCCCGG	GAAAACACAG	1080
AGAGACTGCA	ATCAGGCATC	TCATAGTCCA	TGGTTTTCAG	ATAGGAGGAT	GGTCAACTCT	1140
ATCATTGTTG	TTGACAAAGG	CTTAAACTCA	ATTCCAAAAT	TGAAGGTATG	GACGATATCT	1200
ATGAGACAGA	ATTACTGGGG	GTCAGAAGGA	AGGTTACTTC	TACTAGGTAA	CAAGATCTAT	1260
ATATATACAA	GATCCACAAG	TTGGCATAGC	AAGTTACAAT	TAGGAATAAT	TGATATTACT	1320
GATTACAGTG	ATATAAGGAT	AAAATGGACA	TGGCATAATG	TGCTATCAAG	ACCAGGAAAC	1380

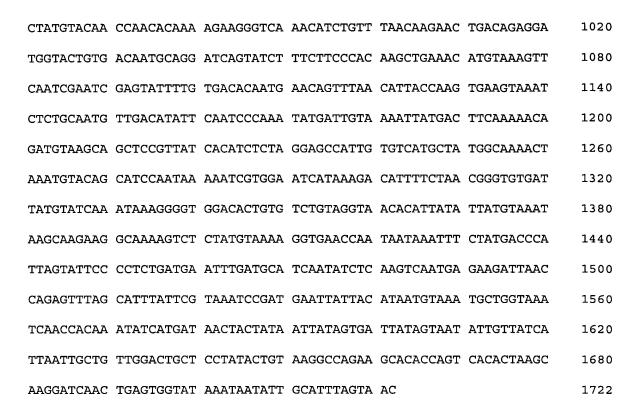
AATGAATGTC CATGGGGACA TTCATGTCCA GATGGATGTA TAACAGGAGT ATATACTGAT 1440
GCATATCCAC TCAATCCCAC AGGGAGCATT GTGTCATCTG TCATATTAGA TTCACAAAAA 1500
TCGAGAGTGA ACCCAGTCAT AACTTACTCA ACAGCAACCG AAAGAGTAAA CGAGCTGGCC 1560
ATCCGAAACA GAACACTCTC AGCTGGATAT ACAACAACAA GCTGCATCAC ACACTATAAC 1620
AAAGGATATT GTTTCATAT AGTAGAAATA AATCAGAAAA GCTTAAACAC ACTTCAACCC 1680
ATGTTGTTCA AGACAGAGGT TCCAAAAAGC TGCAG 1715

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1722 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGGAGTTGC	CAATCCTCAA	AGCAAATGCA	ATTACCACAA	TCCTCGCTGC	AGTCACATTT	60
TGCTTTGCTT	CTAGTCAAAA	CATCACTGAA	GAATTTTATC	AATCAACATG	CAGTGCAGTT	120
AGCAAAGGCT	ATCTTAGTGC	TCTAAGAACT	GGTTGGTATA	CTAGTGTTAT	AACTATAGAA	180
TTAAGTAATA	TCAAGGAAAA	TAAGTGTAAT	GGAACAGATG	CTAAGGTAAA	ATTGATGAAA	240
CAAGAATTAG	ATAAATATAA	AAATGCTGTA	ACAGAATTGC	AGTTGCTCAT	GCAAAGCACA	300
CCAGCAGCAA	ACAATCGAGC	CAGAAGAGAA	CTACCAAGGT	TTATGAATTA	TACACTCAAC	360
AATACCAAAA	AAACCAATGT	AACATTAAGC	AAGAAAAGGA	AAAGAAGATT	TCTTGGTTTT	420
TTGTTAGGTG	TTGGATCTGC	AATCGCCAGT	GGCATTGCTG	TATCTAAGGT	CCTGCACTTA	480
GAAGGAGAAG	TGAACAAGAT	CAAAAGTGCT	CTACTATCCA	CAAACAAGGC	CGTAGTCAGC	540
TTATCAAATG	GAGTTAGTGT	CTTAACCAGC	AAAGTGTTAG	ACCTCAAAAA	CTATATAGAT	600
AAACAATTGT	TACCTATTGT	GAATAAGCAA	AGCTGCAGAA	TATCAAATAT	AGAAACTGTG	660
ATAGAGTTCC	AACAAAAGAA	CAACAGACTA	CTAGAGATTA	CCAGGGAATT	TAGTGTTAAT	720
GCAGGTGTAA	CTACACCTGT	AAGCACTTAC	ATGTTAACTA	ATAGTGAATT	ATTGTCATTA	780
ATCAATGATA	TGCCTATAAC	AAATGATCAG	AAAAAGTTAA	TGTCCAACAA	TGTTCAAATA	840
GTTAGACAGC	AAAGTTACTC	TATCATGTCC	ATAATAAAAG	AGGAAGTCTT	AGCATATGTA	900
GTACAATTAC	CACTATATGG	TGTGATAGAT	ACACCTTGTT	GGAAATTACA	CACATCCCCT	960



(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 894 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

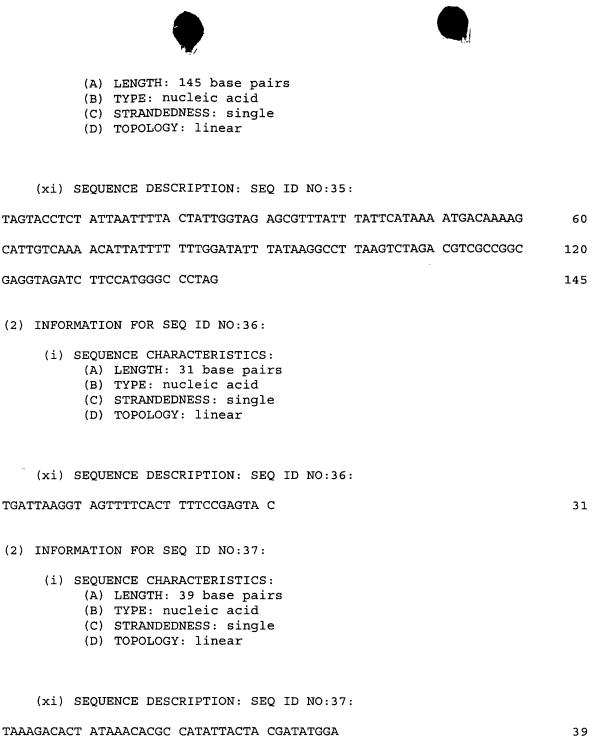
ATGTCCAAAA	ACAAGGACCA	ACGCACCGCT	AAGACACTAG	AAAAGACCTG	GGACACTCTC	60
AATCATTTAT	TATTCATATC	ATCGGGCTTA	TATAAGTTAA	ATCTTAAATC	TGTAGCACAA	120
ATCACATTAT	CCATTCTGGC	AATGATAATC	TCAACTTCAC	TTATAATTAC	AGCCATCATA	180
TTCATAGCCT	CGGCAAACCA	CAAAGTCACA	CTAACAACTG	CAATCATACA	AGATGCAACA	240
AGCCAGATCA	AGAACACAAC	CCCAACATAC	CTCACTCAGG	ATCCTCAGCT	TGGAATCAGC	300
TTCTCCAATC	TGTCTGAAAT	TACATCACAA	ACCACCACCA	TACTAGCTTC	AACAACACCA	360
GGAGTCAAGT	CAAACCTGCA	ACCCACAACA	GTCAAGACTA	AAAACACAAC	AACAACCCAA	420
ACACAACCCA	GCAAGCCCAC	TACAAAACAA	CGCCAAAACA	AACCACCAAA	CAAACCCAAT	480
AATGATTTTC	ACTTCGAAGT	GTTTAACTTT	GTACCCTGCA	GCATATGCAG	CAACAATCCA	540

CTGGG	CTATCTGCAA	AAGAATACCA	AACAAAAAAC	CAGGAAAGAA	AACCACCACC	600
CTACAA	AAAAACCAAC	CTTCAAGACA	ACCAAAAAAG	ATCTCAAACC	TCAAACCACT	660
CAAAGG	AAGTACCCAC	CACCAAGCCC	ACAGAAGAGC	CAACCATCAA	CACCACCAAA	720
ACATCA	CAACTACACT	GCTCACCAAC	AACACCACAG	GAAATCCAAA	ACTCACAAGT	780
rggaaa	CCTTCCACTC	AACCTCCTCC	GAAGGCAATC	TAAGCCCTTC	TCAAGTCTCC	840
CATCCG	AGCACCCATC	ACAACCCTCA	TCTCCACCCA	ACACAACACG	CCAG	894
(i) SE	EQUENCE CHAP (A) LENGTH: (B) TYPE: nu (C) STRANDEI	RACTERISTICS 32 base paracleic acid DNESS: singl	S: irs			
	-			:		32
,	(A) LENGTH: (B) TYPE: nu (C) STRANDEI	17 base par cleic acid ONESS: sing	irs			
(xi) SI	EQUENCE DESC	CRIPTION: SI	EQ ID NO:30	:		
TGAACTATTA CTCCTAG						17
(i) SI	EQUENCE CHAP (A) LENGTH: (B) TYPE: nu (C) STRANDEI	RACTERISTICS 85 base pa: 1cleic acid DNESS: sing	S: irs			
	CTACAA CAAAGG ACATCA CGGAAA CATCCG INFORMA (i) SI CTATTA CTATTA INFORMA (i) SI CTATTA INFORMA (i) SI	CTACAA AAAAACCAAC CAAAGG AAGTACCCAC ACATCA CAACTACACT GGAAA CCTTCCACTC CATCCG AGCACCCATC INFORMATION FOR SE (i) SEQUENCE CHAE (A) LENGTH: (B) TYPE: nu (C) STRANDEI (D) TOPOLOGY (xi) SEQUENCE CHAE (A) LENGTH: (B) TYPE: nu (C) STRANDEI (D) TOPOLOGY (xi) SEQUENCE CHAE (A) LENGTH: (B) TYPE: nu (C) STRANDEI (D) TOPOLOGY (xi) SEQUENCE DESC	CTACAA AAAAACCAAC CTTCAAGACA CAAAGG AAGTACCCAC CACCAAGCCC ACATCA CAACTACACT GCTCACCAAC TGGAAA CCTTCCACTC AACCTCCTCC CATCCG AGCACCCATC ACAACCCTCA INFORMATION FOR SEQ ID NO:29 (i) SEQUENCE CHARACTERISTICS (A) LENGTH: 32 base pa: (B) TYPE: nucleic acid (C) STRANDEDNESS: sing: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SI CATTAGT TTCCAGGACA CTATTATCCT INFORMATION FOR SEQ ID NO:30 (i) SEQUENCE CHARACTERISTICS (A) LENGTH: 17 base pa: (B) TYPE: nucleic acid (C) STRANDEDNESS: sing: (D) TOPOLOGY: linear (xi) SEQUENCE CHARACTERISTICS (A) LENGTH: 17 base pa: (B) TYPE: nucleic acid (C) STRANDEDNESS: sing: (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SI CTATTA CTCCTAG INFORMATION FOR SEQ ID NO:31 (i) SEQUENCE CHARACTERISTICS (A) LENGTH: 85 base pa: (B) TYPE: nucleic acid	CTACAA AAAAACCAAC CTTCAAGACA ACCAAAAAAG CAAAGG AAGTACCCAC CACCAAGCCC ACAGAAGAGC ACATCA CAACTACACT GCTCACCAAC AACACCACAG RGGAAA CCTTCCACTC AACCTCCTCC GAAGGCAATC CATCCG AGCACCCATC ACAACCCTCA TCTCCACCCA RIFORMATION FOR SEQ ID NO:29: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29: CITAGT TTCCAGGACA CTATTATCCT AG INFORMATION FOR SEQ ID NO:30: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: CTATTA CTCCTAG INFORMATION FOR SEQ ID NO:31: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	TTACAA AAAAACCAAC CTTCAAGACA ACCAAAAAAG ATCTCAAACC CAAAGG AAGTACCCAC CACCAAGCCC ACAGAAGAGC CAACCATCAA ACATCA CAACTACACT GCTCACCAAC AACACCACAG GAAATCCAAA TGGAAA CCTTCCACTC AACCTCCTCC GAAGGCAATC TAAGCCCTTC CATCCG AGCACCCATC ACAACCCTCA TCTCCACCCA ACACAACACG INFORMATION FOR SEQ ID NO:29: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29: STTAGT TTCCAGGACA CTATTATCCT AG INFORMATION FOR SEQ ID NO:30: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: CTATTA CTCCTAG INFORMATION FOR SEQ ID NO:31: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TYPE: nucleic acid (C) STRANDEDNESS: single	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29: STTAGT TTCCAGGACA CTATTATCCT AG INFORMATION FOR SEQ ID NO:30: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: CTATTA CTCCTAG INFORMATION FOR SEQ ID NO:31: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 85 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AACAAAACGA AGACCAAGAT TCCAG	85
(2) INFORMATION FOR SEQ ID NO:32:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CGTAGTTAGA TCGTGATGTA CTCCTAG	27
(2) INFORMATION FOR SEQ ID NO:33:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 136 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
GTACGGTTGA AATTATGACG ATTAATAATG TTGTTACTAA TACCGTAGAA GGACGGTTTA	60
TCTATAGTGT TTTGATGTCG TACATCCACA TAACCAGTTG TCAGGGTTTC CCTACTTCTA	120
TAGTGTTTTG AAGCTT	136
(2) INFORMATION FOR SEQ ID NO:34:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 98 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
TAGTACCTCT ATTAATTTTA CTATTGGTAG AGCGTTTATT TATTCATAAA ATGACAAAAG	60
CATTGTCAAA ACATTATTTT TTTGGATATT TATCTTAA	98
(2) INFORMATION FOR SEQ ID NO:35:	

(i) SEQUENCE CHARACTERISTICS:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TAAAGACACT ATAAACACGC CATATTACTA CGATATGGA

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:



